



SEQUENCE LISTING

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STRUCK, JOACHIM
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<120> USES OF CARBAMOYL PHOSPHATE SYNTHETASE 1 (CPS 1) AND
ITS FRAGMENTS FOR THE DIAGNOSIS OF INFLAMMATORY
DISEASES AND SEPSIS

<130> 121778-04341933

<140> 10/511,756

<141> 2005-05-25

<150> PCT/EP03/03939

<151> 2003-04-15

<150> EP 020088415

<151> 2002-04-19

<160> 8

<170> PatentIn Ver. 2.1

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 Arg Pro Gly Ile Arg Leu Leu Ser Val Lys Ala Gln Thr Ala His Ile
 35 40 45
 Val Leu Glu Asp Gly Thr Lys Met Lys Gly Tyr Ser Phe Gly His Pro
 50 55 60
 Ser Ser Val Ala Gly Glu Val Val Phe Asn Thr Gly Leu Gly Gly Tyr
 65 70 75 80
 Pro Glu Ala Ile Thr Asp Pro Ala Tyr Lys Gly Gln Ile Leu Thr Met
 85 90 95
 Ala Asn Pro Ile Ile Gly Asn Gly Gly Ala Pro Asp Thr Thr Ala Leu
 100 105 110
 Asp Glu Leu Gly Leu Ser Lys Tyr Leu Glu Ser Asn Gly Ile Lys Val
 115 120 125
 Ser Gly Leu Leu Val Leu Asp Tyr Ser Lys Asp Tyr Asn His Trp Leu
 130 135 140
 Ala Thr Lys Ser Leu Gly Gln Trp Leu Gln Glu Glu Lys Val Pro Ala
 145 150 155 160

Ile	Tyr	Gly	Val	Asp	Thr	Arg	Met	Leu	Thr	Lys	Ile	Ile	Arg	Asp	Lys	165	170	175	
Gly	Thr	Met	Leu	Gly	Lys	Ile	Glu	Phe	Glu	Gly	Gln	Pro	Val	Asp	Phe	180	185	190	
Val	Asp	Pro	Asn	Lys	Gln	Asn	Leu	Ile	Ala	Glu	Val	Ser	Thr	Lys	Asp	195	200	205	
Val	Lys	Val	Tyr	Gly	Lys	Gly	Asn	Pro	Thr	Lys	Val	Val	Ala	Val	Asp	210	215	220	
Cys	Gly	Ile	Lys	Asn	Asn	Val	Ile	Arg	Leu	Leu	Val	Lys	Arg	Gly	Ala	225	230	235	240
Glu	Val	His	Leu	Val	Pro	Trp	Asn	His	Asp	Phe	Thr	Lys	Met	Glu	Tyr	245	250	255	
Asp	Gly	Ile	Leu	Ile	Ala	Gly	Gly	Pro	Gly	Asn	Pro	Ala	Leu	Ala	Glu	260	265	270	
Pro	Leu	Ile	Gln	Asn	Val	Arg	Lys	Ile	Leu	Glu	Ser	Asp	Arg	Lys	Glu	275	280	285	
Pro	Leu	Phe	Gly	Ile	Ser	Thr	Gly	Asn	Leu	Ile	Thr	Gly	Leu	Ala	Ala	290	295	300	
Gly	Ala	Lys	Thr	Tyr	Lys	Met	Ser	Met	Ala	Asn	Arg	Gly	Gln	Asn	Gln	305	310	315	320
Pro	Val	Leu	Asn	Ile	Thr	Asn	Lys	Gln	Ala	Phe	Ile	Thr	Ala	Gln	Asn	325	330	335	
His	Gly	Tyr	Ala	Leu	Asp	Asn	Thr	Leu	Pro	Ala	Gly	Trp	Lys	Pro	Leu	340	345	350	
Phe	Val	Asn	Val	Asn	Asp	Gln	Thr	Asn	Glu	Gly	Ile	Met	His	Glu	Ser	355	360	365	
Lys	Pro	Phe	Phe	Ala	Val	Gln	Phe	His	Pro	Glu	Val	Thr	Pro	Gly	Pro	370	375	380	
Ile	Asp	Thr	Glu	Tyr	Leu	Phe	Asp	Ser	Phe	Phe	Ser	Leu	Ile	Lys	Lys	385	390	395	400
Gly	Lys	Ala	Thr	Thr	Ile	Thr	Ser	Val	Leu	Pro	Lys	Pro	Ala	Leu	Val	405	410	415	
Ala	Ser	Arg	Val	Glu	Val	Ser	Lys	Val	Leu	Ile	Leu	Gly	Ser	Gly	Gly	420	425	430	
Leu	Ser	Ile	Gly	Gln	Ala	Gly	Glu	Phe	Asp	Tyr	Ser	Gly	Ser	Gln	Ala	435	440	445	
Val	Lys	Ala	Met	Lys	Glu	Glu	Asn	Val	Lys	Thr	Val	Leu	Met	Asn	Pro	450	455	460	

Asn	Ile	Ala	Ser	Val	Gln	Thr	Asn	Glu	Val	Gly	Leu	Lys	Gln	Ala	Asp	465	470	475	480
Thr	Val	Tyr	Phe	Leu	Pro	Ile	Thr	Pro	Gln	Phe	Val	Thr	Glu	Val	Ile	485	490	495	
Lys	Ala	Glu	Gln	Pro	Asp	Gly	Leu	Ile	Leu	Gly	Met	Gly	Gly	Gln	Thr	500	505	510	
Ala	Leu	Asn	Cys	Gly	Val	Glu	Leu	Phe	Lys	Arg	Gly	Val	Leu	Lys	Glu	515	520	525	
Tyr	Gly	Val	Lys	Val	Leu	Gly	Thr	Ser	Val	Glu	Ser	Ile	Met	Ala	Thr	530	535	540	
Glu	Asp	Arg	Gln	Leu	Phe	Ser	Asp	Lys	Leu	Asn	Glu	Ile	Asn	Glu	Lys	545	550	555	560
Ile	Ala	Pro	Ser	Phe	Ala	Val	Glu	Ser	Ile	Glu	Asp	Ala	Leu	Lys	Ala	565	570	575	
Ala	Asp	Thr	Ile	Gly	Tyr	Pro	Val	Met	Ile	Arg	Ser	Ala	Tyr	Ala	Leu	580	585	590	
Gly	Gly	Leu	Gly	Ser	Gly	Ile	Cys	Pro	Asn	Arg	Glu	Thr	Leu	Met	Asp	595	600	605	
Leu	Ser	Thr	Lys	Ala	Phe	Ala	Met	Thr	Asn	Gln	Ile	Leu	Val	Glu	Lys	610	615	620	
Ser	Val	Thr	Gly	Trp	Lys	Glu	Ile	Glu	Tyr	Glu	Val	Val	Arg	Asp	Ala	625	630	635	640
Asp	Asp	Asn	Cys	Val	Thr	Val	Cys	Asn	Met	Glu	Asn	Val	Asp	Ala	Met	645	650	655	
Gly	Val	His	Thr	Gly	Asp	Ser	Val	Val	Val	Ala	Pro	Ala	Gln	Thr	Leu	660	665	670	
Ser	Asn	Ala	Glu	Phe	Gln	Met	Leu	Arg	Arg	Thr	Ser	Ile	Asn	Val	Val	675	680	685	
Arg	His	Leu	Gly	Ile	Val	Gly	Glu	Cys	Asn	Ile	Gln	Phe	Ala	Leu	His	690	695	700	
Pro	Thr	Ser	Met	Glu	Tyr	Cys	Ile	Ile	Glu	Val	Asn	Ala	Arg	Leu	Ser	705	710	715	720
Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr	Gly	Tyr	Pro	Leu	Ala	Phe	725	730	735	
Ile	Ala	Ala	Lys	Ile	Ala	Leu	Gly	Ile	Pro	Leu	Pro	Glu	Ile	Lys	Asn	740	745	750	
Val	Val	Ser	Gly	Lys	Thr	Ser	Ala	Cys	Phe	Glu	Pro	Ser	Leu	Asp	Tyr	755	760	765	

Met	Val	Thr	Lys	Ile	Pro	Arg	Trp	Asp	Leu	Asp	Arg	Phe	His	Gly	Thr	
770						775					780					
Ser	Ser	Arg	Ile	Gly	Ser	Ser	Met	Lys	Ser	Val	Gly	Glu	Val	Met	Ala	
785					790					795					800	
Ile	Gly	Arg	Thr	Phe	Glu	Glu	Ser	Phe	Gln	Lys	Ala	Leu	Arg	Met	Cys	
				805					810					815		
His	Pro	Ser	Ile	Glu	Gly	Phe	Thr	Pro	Arg	Leu	Pro	Met	Asn	Lys	Glu	
			820					825					830			
Trp	Pro	Ser	Asn	Leu	Asp	Leu	Arg	Lys	Glu	Leu	Ser	Glu	Pro	Ser	Ser	
		835					840					845				
Thr	Arg	Ile	Tyr	Ala	Ile	Ala	Lys	Ala	Ile	Asp	Asp	Asn	Met	Ser	Leu	
	850					855					860					
Asp	Glu	Ile	Glu	Lys	Leu	Thr	Tyr	Ile	Asp	Lys	Trp	Phe	Leu	Tyr	Lys	
865					870					875					880	
Met	Arg	Asp	Ile	Leu	Asn	Met	Glu	Lys	Thr	Leu	Lys	Gly	Leu	Asn	Ser	
				885					890					895		
Glu	Ser	Met	Thr	Glu	Glu	Thr	Leu	Lys	Arg	Ala	Lys	Glu	Ile	Gly	Phe	
			900					905					910			
Ser	Asp	Lys	Gln	Ile	Ser	Lys	Cys	Leu	Gly	Leu	Thr	Glu	Ala	Gln	Thr	
		915					920					925				
Arg	Glu	Leu	Arg	Leu	Lys	Lys	Asn	Ile	His	Pro	Trp	Val	Lys	Gln	Ile	
	930					935					940					
Asp	Thr	Leu	Ala	Ala	Glu	Tyr	Pro	Ser	Val	Thr	Asn	Tyr	Leu	Tyr	Val	
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Thr	Tyr	Asn	Gly	Gln	Glu	His	Asp	Val	Asn	Phe	Asp	Asp	His	Gly	Met	
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Met	Val	Leu	Gly	Cys	Gly	Pro	Tyr	His	Ile	Gly	Ser	Ser	Val	Glu	Phe	
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Asp	Trp	Cys	Ala	Val	Ser	Ser	Ile	Arg	Thr	Leu	Arg	Gln	Leu	Gly	Lys	
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Leu	Asp	Ile	Tyr	His	Gln	Glu	Ala	Cys	Gly	Gly	Cys	Ile	Ile	Ser	Val	
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Val Lys Ile Met Gly Thr Ser Pro Leu Gln Ile Asp Arg Ala Glu Asp
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 Arg Ser Ile Phe Ser Ala Val Leu Asp Glu Leu Lys Val Ala Gln Ala
 1090 1095 1100
 Pro Trp Lys Ala Val Asn Thr Leu Asn Glu Ala Leu Glu Phe Ala Lys
 1105 1110 1115 1120
 Ser Val Asp Tyr Pro Cys Leu Leu Arg Pro Ser Tyr Val Leu Ser Gly
 1125 1130 1135
 Ser Ala Met Asn Val Val Phe Ser Glu Asp Glu Met Lys Lys Phe Leu
 1140 1145 1150
 Glu Glu Ala Thr Arg Val Ser Gln Glu His Pro Val Val Leu Thr Lys
 1155 1160 1165
 Phe Val Glu Gly Ala Arg Glu Val Glu Met Asp Ala Val Gly Lys Asp
 1170 1175 1180
 Gly Arg Val Ile Ser His Ala Ile Ser Glu His Val Glu Asp Ala Gly
 1185 1190 1195 1200
 Val His Ser Gly Asp Ala Thr Leu Met Leu Pro Thr Gln Thr Ile Ser
 1205 1210 1215
 Gln Gly Ala Ile Glu Lys Val Lys Asp Ala Thr Arg Lys Ile Ala Lys
 1220 1225 1230
 Ala Phe Ala Ile Ser Gly Pro Phe Asn Val Gln Phe Leu Val Lys Gly
 1235 1240 1245
 Asn Asp Val Leu Val Ile Glu Cys Asn Leu Arg Ala Ser Arg Ser Phe
 1250 1255 1260
 Pro Phe Val Ser Lys Thr Leu Gly Val Asp Phe Ile Asp Val Ala Thr
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 Lys Val Met Ile Gly Glu Asn Val Asp Glu Lys His Leu Pro Thr Leu
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 Asp His Pro Ile Ile Pro Ala Asp Tyr Val Ala Ile Lys Ala Pro Met
 1300 1305 1310
 Phe Ser Trp Pro Arg Leu Arg Asp Ala Asp Pro Ile Leu Arg Cys Glu
 1315 1320 1325
 Met Ala Ser Thr Gly Glu Val Ala Cys Phe Gly Glu Gly Ile His Thr
 1330 1335 1340
 Ala Phe Leu Lys Ala Met Leu Ser Thr Gly Phe Lys Ile Pro Gln Lys
 1345 1350 1355 1360
 Gly Ile Leu Ile Gly Ile Gln Gln Ser Phe Arg Pro Arg Phe Leu Gly
 1365 1370 1375

Val Ala Glu Gln Leu His Asn Glu Gly Phe Lys Leu Phe Ala Thr Glu
1380 1385 1390

Ala Thr Ser Asp Trp Leu Asn Ala Asn Asn Val Pro Ala Thr Pro Val
1395 1400 1405

Ala Trp Pro Ser Gln Glu Gly Gln Asn Pro Ser Leu Ser Ser Ile Arg
1410 1415 1420

Lys Leu Ile Arg Asp Gly Ser Ile Asp Leu Val Ile Asn Leu Pro Asn
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Asn Asn Thr Lys Phe Val His Asp Asn Tyr Val Ile Arg Arg Thr Ala
1445 1450 1455

Val Asp Ser Gly Ile Pro Leu Leu Thr Asn Phe Gln Val Thr Lys Leu
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Phe Ala Glu Ala Val Gln Lys Ser Arg Lys Val Asp Ser Lys Ser Leu
1475 1480 1485

Phe His Tyr Arg Gln Tyr Ser Ala Gly Lys Ala Ala
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Asn

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<213> Artificial Sequence

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